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1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/976,451

DATE: 02/12/2002
TIME: 12:05:54

Input Set : A:\Pm4968.txt
Output Set: N:\CRF3\02122002\I976451.raw

4 <110> APPLICANT: Braun, Jonathan
5 Wei, Bo
6 Forbes, Ashley
8 <120> TITLE OF INVENTION: Methods of Diagnosing and Treating
9 Crohn's Disease Using Pseudomonas Antigens
12 <130> FILE REFERENCE: P-PM 4968
14 <140> CURRENT APPLICATION NUMBER: US 09/976,451
15 <141> CURRENT FILING DATE: 2001-10-12
17 <150> PRIOR APPLICATION NUMBER: US 60/240,347
18 <151> PRIOR FILING DATE: 2000-10-13
20 <160> NUMBER OF SEQ ID NOS: 10
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 551
26 <212> TYPE: DNA
27 <213> ORGANISM: P. fluorescens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)...(549)
33 <400> SEQUENCE: 1
34 atg acg gaa cca gta tcc aca ggc agg tgc gat tca ccc ctt ctc
35 Met Thr Glu Pro Val Ser Thr Gly Arg Cys Asp Ser Pro Leu Leu
36 1 5 10 15
38 gcg ttc gtc gac aat cga ctg att ctg gtg aag atc gtc gcc cgt
39 Ala Phe Val Asp Asn Arg Leu Ile Leu Val Lys Ile Ala Ala Arg
40 20 25 30
42 acc ggg tgc cgc tcc cgc gcc gaa gac gtc gtc cag gac gcc tac
43 Thr Gly Cys Arg Ser Arg Ala Glu Asp Val Val Gln Asp Ala Tyr
44 35 40 45
46 cgg ctg cag tcg gcg ccg acc atc acc tca tcg ttc aag gcc caa
47 Arg Leu Gln Ser Ala Pro Thr Ile Thr Ser Ser Phe Lys Ala Gln
48 50 55 60
50 agt tat ctg ttt cag atc gta cgc aac ctg gcg atc gat cat tac
51 Ser Tyr Leu Phe Gln Ile Val Arg Asn Leu Ala Ile Asp His Tyr
52 65 70 75
54 aag cag gcc ctg gag ctc aaa tac tcc ggg acc gaa gag gaa ggc
55 Lys Gln Ala Leu Glu Leu Lys Tyr Ser Gly Thr Glu Glu Glu Gly
56 85 90 95
58 aat gtc gtt att cac ggc gct tca ccg gaa acc tcg cac atc aat
59 Asn Val Val Ile His Gly Ala Ser Pro Glu Thr Ser His Ile Asn
60 100 105 110
62 aac acc ctg gaa aac atc gcc gac gcc ctg acg cca ctg ccc cag
63 Asn Thr Leu Glu Asn Ile Ala Asp Ala Leu Thr Gln Leu Pro Gln

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64	115	120	125	
66	acc cgc tac gcg ttc gag atg tac cgc ttg cat ggc gtg ccg caa aaa			432
67	Thr Arg Tyr Ala Phe Glu Met Tyr Arg Leu His Gly Val Pro Gln Lys			
68	130	135	140	
70	gac atc gcc aag gag ctt ggg gtg tct ccg acc ttg gtg aac ttc atg			480
71	Asp Ile Ala Lys Glu Leu Gly Val Ser Pro Thr Leu Val Asn Phe Met			
72	145	150	155	160
74	att cgc gat gcg ctg gtg cat tgc cgc aag gtg tcg ggc agt cat agc			528
75	Ile Arg Asp Ala Leu Val His Cys Arg Lys Val Ser Gly Ser His Ser			
76	165	170	175	
78	gat acg ttt gcg cggtt ta			551
79	Asp Thr Phe Ala Arg Arg Val			
80	180			
83	<210> SEQ ID NO: 2			
84	<211> LENGTH: 183			
85	<212> TYPE: PRT			
86	<213> ORGANISM: P. fluorescens			
88	<400> SEQUENCE: 2			
89	Met Thr Glu Pro Val Ser Thr Gly Arg Cys Asp Ser Pro Leu Leu Gln			
90	1	5	10	15
91	Ala Phe Val Asp Asn Arg Leu Ile Leu Val Lys Ile Ala Ala Arg Ile			
92	20	25	30	
93	Thr Gly Cys Arg Ser Arg Ala Glu Asp Val Val Gln Asp Ala Tyr Phe			
94	35	40	45	
95	Arg Leu Gln Ser Ala Pro Thr Ile Thr Ser Ser Phe Lys Ala Gln Leu			
96	50	55	60	
97	Ser Tyr Leu Phe Gln Ile Val Arg Asn Leu Ala Ile Asp His Tyr Arg			
98	65	70	75	80
99	Lys Gln Ala Leu Glu Leu Lys Tyr Ser Gly Thr Glu Glu Gly Leu			
100	85	90	95	
101	Asn Val Val Ile His Gly Ala Ser Pro Glu Thr Ser His Ile Asn Phe			
102	100	105	110	
103	Asn Thr Leu Glu Asn Ile Ala Asp Ala Leu Thr Gln Leu Pro Gln Arg			
104	115	120	125	
105	Thr Arg Tyr Ala Phe Glu Met Tyr Arg Leu His Gly Val Pro Gln Lys			
106	130	135	140	
107	Asp Ile Ala Lys Glu Leu Gly Val Ser Pro Thr Leu Val Asn Phe Met			
108	145	150	155	160
109	Ile Arg Asp Ala Leu Val His Cys Arg Lys Val Ser Gly Ser His Ser			
110	165	170	175	
111	Asp Thr Phe Ala Arg Arg Val			
112	180			
115	<210> SEQ ID NO: 3			
116	<211> LENGTH: 184			
117	<212> TYPE: PRT			
118	<213> ORGANISM: P. fluorescens			
120	<400> SEQUENCE: 3			
121	Met Thr Glu Gln Val Ser Thr Ser Lys Cys Asp Ser Pro Leu Leu His			
122	1	5	10	15

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123 Ala Phe Val Asp Asn Arg Leu Ile Leu Val Lys Ile Ala Ala Arg Ile
124 20 25 30
125 Thr Gly Cys Arg Ser Thr Ala Glu Asp Val Val Gln Asp Ala Phe Phe
126 35 40 45
127 Arg Leu Gln Ser Ala Pro Pro Ile Thr Ser Ser Ile Lys Ala Gln Leu
128 50 55 60
129 Ser Tyr Leu Phe Gln Ile Val Arg Asn Leu Ala Ile Asp His Tyr Arg
130 65 70 75 80
131 Lys Gln Ala Leu Glu Gln Lys Tyr Ser Gly Pro Glu Glu Gly Leu
132 85 90 95
133 Asn Val Val Ile Gln Gly Ala Ser Pro Glu Thr Ser His Ile Asn Phe
134 100 105 110
135 Ser Thr Leu Glu Asn Ile Ala Asp Ala Leu Thr Glu Leu Pro Ser Arg
136 115 120 125
137 Thr Arg Tyr Ala Phe Glu Met Tyr Arg Leu His Gly Val Pro Gln Lys
138 130 135 140
139 Asp Ile Ala Lys Glu Leu Gly Val Ser Pro Thr Leu Val Asn Phe Met
140 145 150 155 160
141 Ile Arg Asp Ala Leu Val His Cys Arg Lys Val Ser Gly Ser Arg Arg
142 165 170 175
143 Asp Ala Val Ala Val Gly Arg Arg
144 180
147 <210> SEQ ID NO: 4
148 <211> LENGTH: 597
149 <212> TYPE: DNA
150 <213> ORGANISM: P. fluorescens
152 <220> FEATURE:
153 <221> NAME/KEY: CDS
154 <222> LOCATION: (1)...(594)
156 <400> SEQUENCE: 4
157 atg cgc acc atg gtc gac agt ggc caa ttg acc gac ccc gag agc gcc 48
158 Met Arg Thr Met Val Asp Ser Gly Gln Leu Thr Asp Pro Glu Ser Ala
159 1 5 10 15
161 cgc ggc aag ttg ctg caa acc gcg gct cat ctg ttt cgc aac aag ggt 96
162 Arg Gly Lys Leu Leu Gln Thr Ala Ala His Leu Phe Arg Asn Lys Gly
163 20 25 30
165 ttc gag cgc acc acc gtg cga gat ctg gcc agc gcc gtg ggc atc cag 144
166 Phe Glu Arg Thr Thr Val Arg Asp Leu Ala Ser Ala Val Gly Ile Gln
167 35 40 45
169 tcc ggc agc atc ttt cat cac ttc aag agc aag gat gag ata ttg cgt 192
170 Ser Gly Ser Ile Phe His His Phe Lys Ser Lys Asp Glu Ile Leu Arg
171 50 55 60
173 gcc gtg atg gag gaa acc acc cat tac aac acc gcg atg atg cgc gct 240
174 Ala Val Met Glu Glu Thr Thr His Tyr Asn Thr Ala Met Met Arg Ala
175 65 70 75 80
177 tca ctg gaa gaa gcg agc acg gtg cgc gaa cgc gtg ctg gcg ctg atc 288
178 Ser Leu Glu Glu Ala Ser Thr Val Arg Glu Arg Val Leu Ala Leu Ile
179 85 90 95
181 cgc tgc aag ttg cag tcg atc atg ggc ggc agt ggc gag gcc atg gcg 336

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182	Arg	Cys	Lys	Leu	Gln	Ser	Ile	Met	Gly	Gly	Ser	Gly	Glu	Ala	Met	Ala	
183				100				105							110		
185	gtg	ctg	gtc	tac	gaa	tgg	cgc	tcg	ctg	tcg	gcc	gaa	ggc	cag	gcg	cac	384
186	Val	Leu	Val	Tyr	Glu	Trp	Arg	Ser	Leu	Ser	Ala	Glu	Gly	Gln	Ala	His	
187				115				120							125		
189	gtg	ctg	gcc	ctg	cgt	gac	gtg	tat	gag	cag	atc	tgg	ttg	cag	gta	ctg	432
190	Val	Leu	Ala	Leu	Arg	Asp	Val	Tyr	Glu	Gln	Ile	Trp	Leu	Gln	Val	Leu	
191				130				135							140		
193	ggc	gag	gcc	aag	gcc	gct	ggc	tac	atc	cgg	ggc	gac	gtg	ttt	att	acc	480
194	Gly	Glu	Ala	Lys	Ala	Ala	Gly	Tyr	Ile	Arg	Gly	Asp	Val	Phe	Ile	Thr	
195	145						150			155					160		
197	cgg	cgc	ttc	ctc	acc	ggg	gcc	tta	tcc	tgg	acc	acc	acc	tgg	ttt	cgt	528
198	Arg	Arg	Phe	Leu	Thr	Gly	Ala	Leu	Ser	Trp	Thr	Thr	Thr	Trp	Phe	Arg	
199				165				170							175		
201	gcc	caa	ggc	agc	ctg	acc	ctt	gag	gag	ttg	gcc	gaa	gag	gcc	ttg	ttg	576
202	Ala	Gln	Gly	Ser	Leu	Thr	Leu	Glu	Glu	Leu	Ala	Glu	Glu	Ala	Leu	Leu	
203				180				185							190		
205	atg	gtg	ctg	aag	tcg	gac	tga										597
206	Met	Val	Leu	Lys	Ser	Asp											
207				195													
210	<210>	SEQ	ID	NO:	5												
211	<211>	LENGTH:	198														
212	<212>	TYPE:	PRT														
213	<213>	ORGANISM:	P. fluorescens														
215	<400>	SEQUENCE:	5														
216	Met	Arg	Thr	Met	Val	Asp	Ser	Gly	Gln	Leu	Thr	Asp	Pro	Glu	Ser	Ala	
217	1				5				10						15		
218	Arg	Gly	Lys	Leu	Leu	Gln	Thr	Ala	Ala	His	Leu	Phe	Arg	Asn	Lys	Gly	
219					20				25						30		
220	Phe	Glu	Arg	Thr	Thr	Val	Arg	Asp	Leu	Ala	Ser	Ala	Val	Gly	Ile	Gln	
221					35			40							45		
222	Ser	Gly	Ser	Ile	Phe	His	His	Phe	Lys	Ser	Lys	Asp	Glu	Ile	Leu	Arg	
223					50			55							60		
224	Ala	Val	Met	Glu	Glu	Thr	Thr	His	Tyr	Asn	Thr	Ala	Met	Met	Arg	Ala	
225				65			70			75					80		
226	Ser	Leu	Glu	Glu	Ala	Ser	Thr	Val	Arg	Glu	Arg	Val	Leu	Ala	Leu	Ile	
227					85			90							95		
228	Arg	Cys	Lys	Leu	Gln	Ser	Ile	Met	Gly	Gly	Ser	Gly	Glu	Ala	Met	Ala	
229					100			105							110		
230	Val	Leu	Val	Tyr	Glu	Trp	Arg	Ser	Leu	Ser	Ala	Glu	Gly	Gln	Ala	His	
231				115			120								125		
232	Val	Leu	Ala	Leu	Arg	Asp	Val	Tyr	Glu	Gln	Ile	Trp	Leu	Gln	Val	Leu	
233				130			135								140		
234	Gly	Glu	Ala	Lys	Ala	Ala	Gly	Tyr	Ile	Arg	Gly	Asp	Val	Phe	Ile	Thr	
235				145			150			155					160		
236	Arg	Arg	Phe	Leu	Thr	Gly	Ala	Leu	Ser	Trp	Thr	Thr	Thr	Trp	Phe	Arg	
237					165			170							175		
238	Ala	Gln	Gly	Ser	Leu	Thr	Leu	Glu	Glu	Leu	Ala	Glu	Glu	Ala	Leu	Leu	
239					180			185							190		

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240 Met Val Leu Lys Ser Asp
241 195
244 <210> SEQ ID NO: 6
245 <211> LENGTH: 17
246 <212> TYPE: DNA
247 <213> ORGANISM: P. fluorescens
249 <400> SEQUENCE: 6
250 agatcaagat cacaagc 17
252 <210> SEQ ID NO: 7
253 <211> LENGTH: 187
254 <212> TYPE: PRT
255 <213> ORGANISM: P. aeruginosa
257 <400> SEQUENCE: 7
258 Met Ser Glu Gln Leu Ser Thr Arg Arg Cys Asp Thr Pro Leu Leu Gln
259 1 5 10 15
260 Ala Phe Val Asp Asn Arg Arg Thr Ile Leu Val Lys Ile Ala Ala Arg Ile
261 20 25 30
262 Thr Gly Cys Arg Ser Arg Ala Glu Asp Val Val Gln Asp Ala Phe Phe
263 35 40 45
264 Arg Leu Gln Ser Ala Pro Gln Ile Thr Ser Ser Glu Lys Ala Gln Leu
265 50 55 60
266 Ser Tyr Leu Phe Gln Ile Val Arg Asn Leu Ala Ile Asp His Tyr Arg
267 65 70 75 80
268 Lys Gln Ala Leu Glu Gln Lys Tyr Ser Gly Pro Glu Glu Gly Leu
269 85 90 95
270 Asn Val Val Ile Gln Gly Ala Ser Pro Glu Thr Ser His Ile Asn Tyr
271 100 105 110
272 Ala Thr Leu Glu His Ile Ala Asp Ala Leu Thr Glu Leu Pro Lys Arg
273 115 120 125
274 Thr Arg Tyr Ala Phe Glu Met Tyr Arg Leu His Gly Val Pro Gln Lys
275 130 135 140
276 Asp Ile Ala Lys Glu Leu Gly Val Ser Pro Thr Leu Val Asn Phe Met
277 145 150 155 160
278 Ile Arg Asp Ala Leu Val His Cys Arg Lys Val Thr Ala Glu Arg Gln
279 165 170 175
280 Gly Asp Asn Val Thr His Leu Ser Ala Arg Arg
281 180 185
284 <210> SEQ ID NO: 8
285 <211> LENGTH: 176
286 <212> TYPE: PRT
287 <213> ORGANISM: P. putida
289 <400> SEQUENCE: 8
290 Met Ala Glu Gln Leu Ser Thr Ser Lys Cys Asp Ser Pro Leu Leu Gln
291 1 5 10 15
292 Ala Phe Val Asp Asn Arg Ser Ile Leu Val Lys Ile Ala Ala Arg Ile
293 20 25 30
294 Thr Gly Cys Arg Ser Arg Ala Glu Asp Val Val Gln Asp Ala Phe Phe
295 35 40 45
296 Arg Leu Ser Ala Ala Pro Gln Ile Thr Ser Ser Phe Lys Ala Gln Leu

→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10